Yet further results for lower confidence limits for the abundance of West Greenland minke whales

A. Brandão and D.S. Butterworth

MARAM (Marine Resources Assessment and Management Group)
Department of Mathematics and Applied Mathematics
University of Cape Town, Rondebosch 7701, South Africa

ABSTRACT

The methodology advanced by Brandão and Butterworth (2007 and 2008) for simulating catch sex sampling data in the process of computing lower confidence bounds for the abundance of the West Greenland minke whale population is applied to the modelling scenarios developed at the March 2008 IWC Workshop on Greenlandic Fisheries, also taking account of suggestions made at the subsequent March 2009 Workshop. Calculations have been performed for MSYR = 1% and 2%, and been implemented for Models 3, 4b and 5 for the age-structured population model of Witting and Schweder (2008). For Model 5 for the SW stratum treated as an independent stock, the MLE of pre-exploitation abundance *K* is finite, so that standard likelihood profile estimates of lower confidence bounds for abundance are provided. Two different likelihood formulations are considered, termed **Brandão** and **Schweder**. Results yield lower values for lower bounds on *K* (and on N_{2007}) for Model 3 ("redistribution") than for Model 4b ("influx"). If results for Model 5 for the two strata are added, they are intermediate between those for Models 3 and 4b. Generally, use of the **Brandão likelihood** yields lower values of these lower bounds than does the **Schweder likelihood** function.

INTRODUCTION

This paper reports applications of the methodology set out in IWC (2008a) for the computation of lower confidence limits for the abundance of West Greenland minke whales using an assessment model based upon imbalanced catch sex-ratio data and under the procedures of Brandão and Butterworth (2008) for simulating such catch sex sampling data. The scenarios postulated in Models 3, 4b and 5 of IWC (2008) are investigated using an age structured model (identical to that in Witting and Schweder, 2008) for the resource dynamics. This paper incorporates the suggestions made in the meeting in March 2009 in Copenhagen to further decrease the number non-converging replicates for Model 3. An error in the

formulation of Model 3 has also been corrected to render it identical to that in Witting and Schweder (2008). Further calculations using a likelihood function suggested by Schweder have been implemented in this paper.

DATA

The data used for these analyses are generally identical to those used by Witting and Schweder (2008) but with additional 2007 catches as provided by Witting (*pers. comm*.). For Model 5 the prescriptions of IWC (2008a) were used. Those were incomplete in one respect (the specification for the split of the unsampled whales by stratum and sex for the early Greenlandic period of whaling; the procedures used here to specify these splits are set out in the Appendix).

METHODS

The basic methodology used is the same as that of Brandão and Butterworth (2008) but in this paper only an age-structured population model is used. The population dynamics model is identical to that described in Witting and Schweder (2008). The description of the simulation algorithm and the data generation process is given in the Appendix. Evaluations to deal with new scenarios specified by IWC (2008b) are detailed further below; the basic approach to compute deviance distributions has followed that set out in IWC (2008a), and is not repeated in detail here.

Population dynamics

A sex-structured age-structured model is used:

$$N^{g}_{y+1,0} = 0.5\rho_{y+1}N^{m(f)}_{y+1} \tag{1}$$

$$N^{g}_{y+1,a+1} = (N^{g}_{y,a} - C^{g}_{y,a})\, s_a \qquad 0 \le a \le m\text{-}2 \tag{2}$$

$$N^{g}_{y+1,m} = (N^{g}_{y,m} - C^{g}_{y,m})\, s_m + (N^{g}_{y,m-1} - C^{g}_{y,m-1})\, s_{m-1} \tag{3}$$

where:

g is the gender (male/female) of the minke whale,

$N_{y,a}$ is the total number of minke whales of age a in year y, which is given by:

$N_{y,a} = N^m_{y,a} + N^f_{y,a}$,

$N^g_{y,a}$ is the total number minke whales of gender *g* of age *a* in year *y*,

$C^g_{y,a}$ is the number of West Greenland minke whales of gender *g* of age *a* caught in year *y*,

ρ_{y+1} is the fecundity rate for year *y*+1, which takes the Pella-Tomlinson form:

$$\rho_{y+1} = b_k + [b_{\max} - b_k]\left[1 - \left(N^{1+}_{y+1} / K^{1+}\right)^z\right], \text{ where}$$

b_k is the birth rate at carrying capacity *K*,

b_{max} is the maximal birth rate,

z relates to the strength of density dependence (the degree of compensation parameter).

N^{1+}_{y+1} is the total number of the one plus component of the minke whales population in year *y*+1 given by:

$$N^{1+}_{y+1} = \sum_{a=1}^{m}\left(N^f_{y+1,a} + N^m_{y+1,a}\right),$$

K^{1+} is the carrying capacity of the one plus component of the minke whales population given by:

$$K^{1+} = \sum_{a=1}^{m}\left(N^f_{1948,a} + N^m_{1948,a}\right),$$

$N^{m(f)}_{y+1}$ is the number of mature females at the start of year *y*+1, given by:

$N^{m(f)}_{y+1} = \sum \gamma_a N^f_{y+1,a}$, where

$\gamma_a = \begin{cases} 0 & a < a_m \\ 1 & a \geq a_m \end{cases}$, where a_m is the age of reproductive maturity,

m is the maximum age considered (i.e. the "plus group").

s_a is the age specific annual survival rate, given by:

$$s_a = \begin{cases} s_{juv}s_{ad} & a = 0 \\ s_{juv} & 1 \leq a \leq a_{ad} \\ s_{ad} & a > a_{ad} \end{cases}, \text{ where:}$$

s_{juv} is the survival rate for juveniles,

s_{ad} is the survival rate for adults, and

a_{ad} is the greatest age at which the "juvenile' survival rate applies (taken as $a_{ad} = 1$).

The number of whales of gender *g* of age *a* caught in year *y* is given by:

$$C_{y,a}^{g} = C_{y}^{g} \frac{G_a N_{y,a}^{g}}{\sum_{a'=0}^{m} G_a N_{y,a'}^{g}} \tag{4}$$

where:

G_a is the age-specific differentiation of the catch relative to the age composition of the overall population, given by:

$$G_a = \begin{cases} 0 & a = 0 \\ a/a_c & a < a_c \\ 1 & a \geq a_c \end{cases}$$, where a_c is the age at full recruitment, and

C_y^g is the total catch of minke whales of gender *g* in year *y*.

The initial numbers for each gender *g* at each age *a* are taken to follow an unexploited equilibrium distribution evaluated as follows:

$$N_{1948,a}^{g} = \frac{1}{2} \eta N_a^* \tag{5}$$

where:

$$\eta = \frac{K}{\sum_{a=0}^{m} N_a^*},$$

$$N_a^* = \begin{cases} 1 & a = 0 \\ s_{a-1} N_{a-1}^* & 0 < a \leq m-1. \\ \frac{s_m N_{m-1}^*}{1 - s_m} & a = m \end{cases}$$

The total number of minke whales caught in the whaling period *i* in year *y* is given by:

$$C_{y}^{i} = C_{y}^{m(i)} + C_{y}^{f(i)} \tag{6}$$

where:

$C_y^{m(i)}$ is the number of male minke whales caught in period *i* by the fishery concerned, where the period/fishery *i* represents:

$$i = \begin{cases} I & \text{the period } 1955-1978 \text{ by Greenlanic whalers} \\ II & \text{the period } 1968-1985 \text{ by Norwegian whalers, and} \\ III & \text{the period } 1987-2006 \text{ by Greenlanic whalers} \end{cases}$$

$C_y^{f(i)}$ is the corresponding number of female minke whales caught in period/fishery *i*.

For the simplest form of the model (Model 5), the expected number of female minke whales caught by each period/fishery *i* in year *y* is given by:

$$\hat{C}_y^{f(i)} = C_y^i \frac{N_y^f}{N_y^f + \lambda^i N_y^m}, \tag{7}$$

where:

λ^i is the selectivity of males relative to females for the period and fishery concerned, and is assumed to remain constant over that period, with equation (6) following from the associated assumptions that:

$$\hat{C}_y^{f(i)} = F_y^{(i)} N_y^f \; ; \; \hat{C}_y^{m(i)} = \lambda^i F_y^{(i)} N_y^m \text{, and} \tag{8}$$

$N_y^{f/m}$ is the total number of minke females/males in year *y*, given by:

$$N_y^{f/m} = \sum_a G_a N_{y,a}^{f/m} \tag{9}$$

The likelihood function

Two likelihood functions are considered in this paper. One is the likelihood function considered previously by Brandão and Butterworth (2007, 2008, 2009), which is calculated assuming that the observed female catches are distributed about their expected value according to an overdispersed Poisson model. The negative of the approximate log-likelihood (ignoring constants) which is minimised in the fitting procedure is thus given by:

$$-\ln L = \sum_{i=I}^{III} \sum_{y=y_i^1}^{y_i^*} \left\{ \frac{1}{\sigma_i^2} \frac{\left(C_y^{f(i)} - \hat{C}_y^{f(i)}\right)^2}{\left(2\hat{C}_y^{f(i)}\right)} + \ln \sigma_i + \ln \sqrt{\hat{C}_y^{f(i)}} \right\} \tag{10}$$

where

y_i^1 is the first year of catches for period i,

y_i^* is the last year of catches for period i,

σ_i measures overdispersion of the distribution of catches compared to a Poisson distribution for which the variance is equal to the expected catch for the period and fishery concerned, whose maximum likelihood estimate is given by:

$$\hat{\sigma}_i = \sqrt{\frac{1}{n_i}\sum_{y=y_i^1}^{y_i^*}\left\{\frac{\left(C_y^{f(i)} - \hat{C}_y^{f(i)}\right)^2}{\hat{C}_y^{f(i)}}\right\}} \qquad (11)$$

n_i is the total number of years in the summation of each whaling period.

Note that the formulation of equation (10) assumes that the Poisson-like catch distribution can be approximated by a normal distribution of the same variance. The estimable parameters of this basic model are λ^{I}, λ^{II}, λ^{III}, σ_I, σ_{II}, σ_{III} and K. To simplify the reference of this likelihood function, it will be referred to in the remainder of this paper as the **Brandão likelihood** function.

The second likelihood function considered was proposed by Schweder at the meeting held in Copenhagen in March 2009 (IWC, 2009). For this each data point is conditioned on the total catch. The negative of the approximate log-likelihood (ignoring constants) which is minimised in the fitting procedure is given by:

$$-\ln L = \sum_{i=I}^{III}\sum_{y=y_i^1}^{y_i^*}\left\{\frac{1}{\sigma_i^2}\frac{\left(C_y^{f(i)} - \hat{C}_y^{f(i)}\right)^2}{\left(2\hat{C}_y^{f(i)}\right)\left(1-\frac{\hat{C}_y^{f(i)}}{C_y^i}\right)} + \ln\sigma_i + \ln\sqrt{\hat{C}_y^{f(i)}\left(1-\frac{\hat{C}_y^{f(i)}}{C_y^i}\right)}\right\} \qquad (12)$$

where the maximum likelihood estimate of the overdispersion (σ_i) is now given by:

$$\hat{\sigma}_i = \sqrt{\frac{1}{n_i}\sum_{y=y_i^1}^{y_i^*}\left\{\frac{\left(C_y^{f(i)} - \hat{C}_y^{f(i)}\right)^2}{\hat{C}_y^{f(i)}\left(1-\frac{\hat{C}_y^{f(i)}}{C_y^i}\right)}\right\}}. \qquad (13)$$

Again, to simplify the reference of this likelihood function, it will be referred to in the remainder of this paper as the **Schweder likelihood** function.

Recent refinements

The approaches above are applied to three scenarios set out in IWC (2008a):

Model 3: A closed population model with time dependence of the fractions of females and of males distributed in the NW + CW and SW strata in the later period of

Greenlandic whaling commencing in 1987. To reflect this variation, the proportions of males and of females in the NW + CW stratum (relative to the NW+CW and SW strata combined) are assumed to change with time during the recent period of Greenlandic whaling as:

$$r_t^{m/f} = e^{\alpha^{m/f} + \beta^{m/f} t} / \left[1 + e^{\alpha^{m/f} + \beta^{m/f} t} \right] \quad (14)$$

with a complementary change in the SW stratum. The time *t* is specified by the standard calendar year.

Model 4b: An "influx" model where the number of male whales in the SW stratum is assumed to be influenced by whales moving in from other areas in recent years. To effect this, the λ parameter is assumed to vary linearly over the period from 1987 (λ_{87}) to 2007 (λ_{07}) when these Greenlandic catches were sampled for sex.

Model 5: The animals in the NW + CW and SW strata are assumed to exhibit site fidelity, and so (*in extremis*) are treated as separate populations with different values of λ for each period and stratum which do not change within those periods.

In other changes from earlier analyses, catch data from the Norwegian fishery period II are not taken into account in the likelihood (except for Model 5 for the NW + CW stratum), but are included amongst the catches taken into account in the population dynamics equations.

Dealing with non-convergence and negative deviances

Brandão and Butterworth (2009) reported on an initial approach to overcome convergence problems by lowering the convergence criterion of the likelihood gradient from less than 0.00001 to less than 0.001. If the gradient was greater than 0.001, the model fit was re-run with initial parameter values set to be those obtained in the last run. Instances of negative deviance were eliminated by initializing the search over parameter values for the model that estimates *K* (i.e. the larger model) with the parameter estimates obtained from the model that sets *K* as fixed (i.e. the smaller model, which is a special case of the larger model). With this approach the parameter search for the larger model starts from a position with a likelihood value equal to that of the smaller model, and thus with an additional estimable parameter *K* will either better the likelihood value or, at worst, have this remain the same. However at the March 2009 Workshop, reservations were raised that this procedure might give biased estimates as there was no initial search over different *K* values. At the workshop, trials which

increased the number of re-runs when a model did not converge produced far fewer non-converging results, as did trials where the model was initialised over a range of different *K* values.

The procedure applied in this paper incorporates a combination of several re-runs and various initialisation values of *K*. The initialisation values for parameters other than *K* are as obtained from the smaller model. The procedure adopted consists of seven different *K* initialisation values, which span the range of *K* values as proportions of the true *K*, with one of these *K*s being the true *K*. For each set, the one with the lowest negative log-likelihood is chosen and convergence checked. If the convergence criterion is not met, the model fitting procedure is re-run with initial parameter values set to be those obtained in the last run and a further set of *K* initialisation values as before. A total of five such re-runs takes place unless the convergence criterion is met.

Sensitivity tests

Witting (pers. comm.) suggested a method of decreasing the number of parameters in Model 3 by one subsequent to the March 2009 Workshop. The details of this suggestion were unclear to the authors so that a simpler way of decreasing the number of parameters in Model 3 (thought to be similar to Witting's suggestion) has been investigated here through sensitivity tests. This has been achieved by setting either the value of β^m or β^f to zero in equation (14); this corresponds to either the proportional distribution of males, or alternatively that for females, not changing over time.

RESULTS AND DISCUSSION

Table 1 gives the negative log-likelihood value as well as Akaike Information Criterion adjusted for the number of parameters estimated relative to the sample size (AIC_c). Only Models 3 and 4b can be compared as they are fitted to the same set of data. The model selected through AIC_c is Model 4b for an MSYR value of 2% when either the **Brandão** or the **Schweder likelihood** function is used, though AIC_c differences in relation to MSYR are so small that alternative MSYR values cannot really be distinguished. Figures 1 and 2 show the model fits to the data for the **Brandão** and **Schweder likelihoods** respectively. Figures 3 and 4 show the normal QQ-plots of the standardised residuals of all models, again for the **Brandão** and **Schweder likelihoods** respectively.

The core results obtained for lower confidence bounds (for N_{2007}, K and their ratio) are reported in Table 2 (for the **Brandão likelihood**) and Table 3 (for the **Schweder likelihood**). Results are shown for the cases of MSYR = 1% and 2%. The process used to determine the bounds from the deviances quantiles is illustrated in Figures 5-10 for the various models, MSYR values and the two likelihood functions used. Figures 11 and 12 give the deviance profile for the model with the lowest $AIC_{c,}$ together with the deviance distribution of the 5% quantile when using the **Brandão** and the **Schweder likelihood** functions respectively. The best estimates of the model parameters under the two likelihoods are listed in Tables 4 and 5. Parameter estimates are given for the MSYR = 2% case only.

In the case of Model 5 for the SW stratum treated as if it were an isolated stock, a finite MLE of K results, so that the simulation approach is not needed to determine lower confidence bounds, and these are instead reported using the standard likelihood profile approach.

The problem of negative deviances does not occur for any of the models with the procedure adopted here. The number of non-convergences for Model 3 has also been reduced drastically. For example, for the MSYR = 2% case, the overall largest number of combined (for the model when K is fixed and for the model when K is estimated) non-converged cases in 1000 replicates is 11 and 12 for the **Brandão** and the **Schweder likelihood** respectively. For the cases where the 2.5%, 5% and 10% quantiles intersect the observed deviance curve, the numbers of non-converged cases for the **Brandão likelihood** are 1, 1 and 0 respectively, and 3, 2 and 0 for the **Schweder likelihood**.

Table 6 reports the lower confidence limits obtained for the two sensitivity tests and Figure 13 shows the intersection of the quantiles and the observed deviance curve.

Comparing the different scenarios, production model results yield lower values for lower bounds on K (and for N_{2007}) for Model 3 (“redistribution”) than for Model 4b (“influx”). If results for Model 5 for the two strata are added, they are intermediate between those for Models 3 and 4b. Generally, use of the **Brandão likelihood** yields lower values of these lower bounds than does the **Schweder likelihood** function.

CONCLUDING REMARK

In Brandão and Butterworth (2007), it was found that for some series, the procedure in the Appendix used to generate the sex-sampled catch yielded results with less variability (in median terms) than the original data, and autocorrelation was introduced into the resampling process to correct for that. Because of time limitations this matter has not been investigated further for the new scenarios; thus, results reported in this document all correspond to setting that autocorrelation to zero.

ACKNOWLEDGMENTS

Lars Witting is thanked for providing the data and for interactions related to the age-structured population model used. This work was supported by the South African National Research Foundation.

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Table 1. Negative log-likelihood values (-ln L) and Akaike's Information Criterion (adjusted for the case when the number of parameters is large relative to the sample size) (AIC_c) for various models under a MSYR value of 1 and 2% and for two different likelihood functions used in the model fitting procedure. Except for Model 5 (SW) values are for the case of $K \rightarrow \infty$ (approximated numerically here by K = 200 000). Model 5 (SW) results correspond to the case where K is estimated. Only Model 3 and Model 4b can be compared. The model selected (between Model 3 and Model 4b) under AIC_c amongst all possible MSYR values for the two likelihood functions used is shown in italics, though note that the ability of this statistic to discriminate between the two MSYR values is minimal.

Likelihood function	MSYR	Model	-ln L	AIC_c
Brandão	**1%**	**Model 3**	111.43	244.07
		Model 4b	112.63	241.20
		Model 5 (NW+CW)	135.58	284.66
		Model 5 (SW) - MLE	39.97	88.94
	2%	**Model 3**	111.42	244.05
		Model 4b	*112.63*	*241.19*
		Model 5 (NW+CW)	135.58	284.65
		Model 5 (SW) - MLE	40.55	90.11
Schweder	**1%**	**Model 3**	112.04	245.30
		Model 4b	113.23	242.39
		Model 5 (NW+CW)	135.61	284.71
		Model 5 (SW) - MLE	41.03	89.92
	2%	**Model 3**	112.04	245.29
		Model 4b	*113.23*	*242.38*
		Model 5 (NW+CW)	135.60	284.70
		Model 5 (SW) - MLE	40.46	91.06
Schweder	**2%**	**Model 3 ($\beta^f = 0$)**	112.04	242.60
		Model 3 ($\beta^m = 0$)	112.12	242.77

Table 2. Lower 2.5%, 5%, 10% and 50% quantiles for the population abundance in 2007 (N_{2007}), the carrying capacity (K) and the current depletion (N_{2007}/K) at the start of 2007 for various models for a MSYR value of 1% and 2% and when the **Brandão likelihood** function is used in the model fitting procedure. The values of 5% (low) correspond to the 0.937th quantile of the deviance distribution, while 5% (high) values represent the 0.964th quantile, and essentially reflect 95% confidence bounds on the 5% quantile. For Model 5 (SW) results are for the likelihood profile method and hence are shown in italics (the values in the 50% columns are then the MLEs). The methods are applied to provide the quantiles for K, and then the corresponding values of N_{2007} (and N_{2007}/K) follow from the MSYR value assumed and the actual catches made.

MSYR		N_{2007}					
		5% (low)	5%	5% (high)	2.5%	10%	50%
1%	**Model 3**	2 324	2 578	3 084	2 070	4 701	92 432
	Model 4b	5 190	6 039	7 351	4 578	10 714	109 126
	Model 5 (NW+CW)*	–	–	–	–	–	–
	Model 5 (SW) - MLE	–	*489*	–	*474*	*508*	*641*
2%	**Model 3**	2 968	3 759	3 953	2 768	5 996	169 395
	Model 4b	5 088	6 700	8 376	4 715	13 404	127 388
	Model 5 (NW+CW)	6 561	9 394	12 923	5 573	15 676	138 769
	Model 5 (SW) - MLE	–	*477*	–	*463*	*494*	*615*

MSYR		N_{2007}/K					
		5% (low)	5%	5% (high)	2.5%	10%	50%
1%	**Model 3**	0.122	0.134	0.157	0.110	0.224	0.877
	Model 4b	0.243	0.273	0.317	0.219	0.411	0.894
	Model 5 (NW+CW)*	–	–	–	–	–	–
	Model 5 (SW) - MLE	–	*0.093*	–	*0.090*	*0.096*	*0.119*
2%	**Model 3**	0.187	0.231	0.241	0.175	0.343	0.973
	Model 4b	0.299	0.374	0.443	0.281	0.601	0.964
	Model 5 (NW+CW)	0.472	0.595	0.699	0.419	0.754	0.977
	Model 5 (SW) - MLE	–	*0.112*	–	*0.109*	*0.115*	*0.142*

MSYR		K					
		5% (low)	5%	5% (high)	2.5%	10%	50%
1%	**Model 3**	19 100	19 300	19 700	18 900	21 000	105 400
	Model 4b	21 400	22 100	23 200	20 900	26 100	122 000
	Model 5 (NW+CW)*	–	–	–	–	–	–
	Model 5 (SW) - MLE	–	5 269	–	5 256	5 284	5 391
2%	**Model 3**	15 900	16 300	16 400	15 800	17 500	174 100
	Model 4b	17 000	17 900	18 900	16 800	22 300	132 200
	Model 5 (NW+CW)	13 900	15 800	18 500	13 300	20 800	142 000
	Model 5 (SW) - MLE	–	*4 273*	–	*4 265*	*4 282*	*4 345*

***** Not evaluated for reasons of time.

Table 3. Lower 2.5%, 5%, 10% and 50% quantiles for the population abundance in 2007 (N_{2007}), the carrying capacity (K) and the current depletion (N_{2007}/K) at the start of 2007 for various models for a MSYR value of 1% and 2% and when the **Schweder likelihood** function is used in the model fitting procedure. The values of 5% (low) corresponds to the 0.937th quantile of the deviance distribution, while 5% (high) values represent the 0.964th quantile, and essentially reflect 95% confidence bounds on the 5% quantile. For Model 5 (SW) results are for the likelihood profile method and hence are shown in italics (the values in the 50% columns are then the MLEs). The methods are applied to provide the quantiles for K, and then the corresponding values of N_{2007} (and N_{2007}/K) follow from the MSYR value assumed and the actual catches made.

MSYR		N_{2007}					
		5% (low)	5%	5% (high)	2.5%	10%	50%
1%	**Model 3**	2 578	3 084	3 835	2 324	5 190	178 537
	Model 4b	5 797	6 279	6 995	4 455	10 828	151 576
	Model 5 (NW+CW)	8 490	10 061	13 458	6 889	18 578	163 450
	Model 5 (SW) - MLE	–	*458*	–	*440*	*479*	*634*
2%	**Model 3**	3 366	3 953	4 715	2 566	6 873	194 937
	Model 4b	5 637	6 526	7 719	4 527	13 130	178 512
	Model 5 (NW+CW)	13 658	14 974	16 255	9 533	20 288	170 105
	Model 5 (SW) - MLE	–	*448*	–	*431*	*467*	*608*

MSYR		N_{2007}/K					
		5% (low)	5%	5% (high)	2.5%	10%	50%
1%	**Model 3**	0.134	0.157	0.189	0.122	0.243	0.934
	Model 4b	0.265	0.282	0.305	0.214	0.413	0.923
	Model 5 (NW+CW)	0.438	0.484	0.563	0.383	0.647	0.948
	Model 5 (SW) - MLE	–	*0.087*	–	*0.084*	*0.091*	*0.118*
2%	**Model 3**	0.209	0.241	0.281	0.198	0.382	0.977
	Model 4b	0.326	0.367	0.417	0.271	0.594	0.974
	Model 5 (NW+CW)	0.715	0.741	0.763	0.600	0.815	0.982
	Model 5 (SW) - MLE	–	*0.105*	–	*0.102*	*0.109*	*0.140*

MSYR		K					
		5% (low)	5%	5% (high)	2.5%	10%	50%
1%	**Model 3**	19 300	19 700	20 300	19 100	21 400	191 200
	Model 4b	21 900	22 300	22 900	20 800	26 200	164 300
	Model 5 (NW+CW)	19 400	20 800	23 900	18 000	28 700	172 400
	Model 5 (SW) - MLE	–	*5 244*	–	*5 229*	*5 261*	*5 386*
2%	**Model 3**	16 100	16 400	16 800	15 700	18 000	199 600
	Model 4b	17 300	17 800	18 504	16 700	22 100	183 200
	Model 5 (NW+CW)	19 100	20 200	21 300	15 900	24 900	173 300
	Model 5 (SW) - MLE	–	*4 257*	–	*4 249*	*4 267*	*4 341*

Table 4. Parameter estimates for overdispersion and male selectivity relative to females for the case of $K \to \infty$ (approximated numerically here by K = 200 000) for various models for a MSYR value of 2% and for the **Brandão likelihood**. Model 5 (SW) results correspond to genuine MLEs and hence are shown in italics.

Parameter	Model 3	Model 4b	Model 5 (NW+CW)	Model 5 (SW)
λ^{I} **(Greenland 1955-1978)**	0.356	0.356	0.394	*0.243*
λ^{II} **(Norwegian)**	—	—	0.372	—
λ^{II} **(Greenland NW+CW 1987-2006)**	0.343	0.359	0.360	—
λ^{III} **(Greenland SW 1987-2006)**	—	—	—	*0.124*
λ_{87} **(Greenland SW 1987-2006)**	—	0.122	—	—
λ_{06} **(Greenland SW 1987-2006)**	—	0.389	—	—
α^{f}	59.73	—	—	—
α^{m}	197.57	—	—	—
β^{f}	-0.029	—	—	—
β^{m}	-0.098	—	—	—
σ_{I} **(Greenland 1955-1978)**	0.814	0.814	0.738	*0.422*
σ_{II} **(Norwegian)**	—	—	1.695	—
σ_{II} **(Greenland NW+CW 1987-2006)**	0.638	0.662	0.662	—
σ_{III} **(Greenland SW 1987-2006)**	0.364	0.370	—	*0.363*

Table 5. Parameter estimates for overdispersion and male selectivity relative to females for the case of $K \to \infty$ (approximated numerically here by K = 200 000) for various models for a MSYR value of 2% and for the **Schweder likelihood**. Model 5 (SW) results correspond to genuine MLEs and hence are shown in italics.

Parameter	Model 3	Model 4b	Model 5 (NW+CW)	Model 5 (SW)
λ^{I} **(Greenland 1955-1978)**	0.356	0.356	0.395	*0.252*
λ^{II} **(Norwegian)**	—	—	0.373	—
λ^{II} **(Greenland NW+CW 1987-2006)**	0.337	0.359	0.360	—
λ^{III} **(Greenland SW 1987-2006)**	—	—	—	*0.123*
λ_{87} **(Greenland SW 1987-2006)**	—	0.139	—	—
λ_{06} **(Greenland SW 1987-2006)**	—	0.376	—	—
α^{f}	4.193	—	—	—
α^{m}	133.53	—	—	—
β^{f}	-0.002	—	—	—
β^{m}	-0.066	—	—	—
σ_{I} **(Greenland 1955-1978)**	1.584	1.584	1.386	*0.896*
σ_{II} **(Norwegian)**	—	—	3.244	—
σ_{II} **(Greenland NW+CW 1987-2006)**	1.220	1.281	1.281	—
σ_{III} **(Greenland SW 1987-2006)**	0.842	0.854	—	*0.811*

Table 6. Lower 2.5%, 5%, 10% and 50% quantiles for the population abundance in 2007 (N_{2007}), the carrying capacity (K) and the current depletion (N_{2007}/K) at the start of 2007 for two sensitivity tests for a MSYR value of 2% and when the **Schweder likelihood** function is used in the model fitting procedure. The values of 5% (low) correspond to the 0.937th quantile of the deviance distribution, while 5% (high) values represent the 0.964th quantile, and essentially reflect 95% confidence bounds on the 5% quantile. The methods are applied to provide the quantiles for K, and then the corresponding values of N_{2007} (and N_{2007}/K) follow from the MSYR value assumed and the actual catches made.

	N_{2007}					
	5% (low)	5%	5% (high)	2.5%	10%	50%
Model 3 ($\beta^f = 0$)	3 168	4 902	6 351	2 566	9 486	195 037
Model 3 ($\beta^m = 0$)	3 563	4 715	5 817	2 968	9 331	188 327

	N_{2007}/K					
	5% (low)	5%	5% (high)	2.5%	10%	50%
Model 3 ($\beta^f = 0$)	0.198	0.290	0.359	0.163	0.484	0.977
Model 3 ($\beta^m = 0$)	0.220	0.281	0.334	0.187	0.478	0.976

	K					
	5% (low)	5%	5% (high)	2.5%	10%	50%
Model 3 ($\beta^f = 0$)	16 000	16 900	17 700	15 700	19 600	199 700
Model 3($\beta^m = 0$)	16 200	16 800	17 400	15 900	19 500	193 000

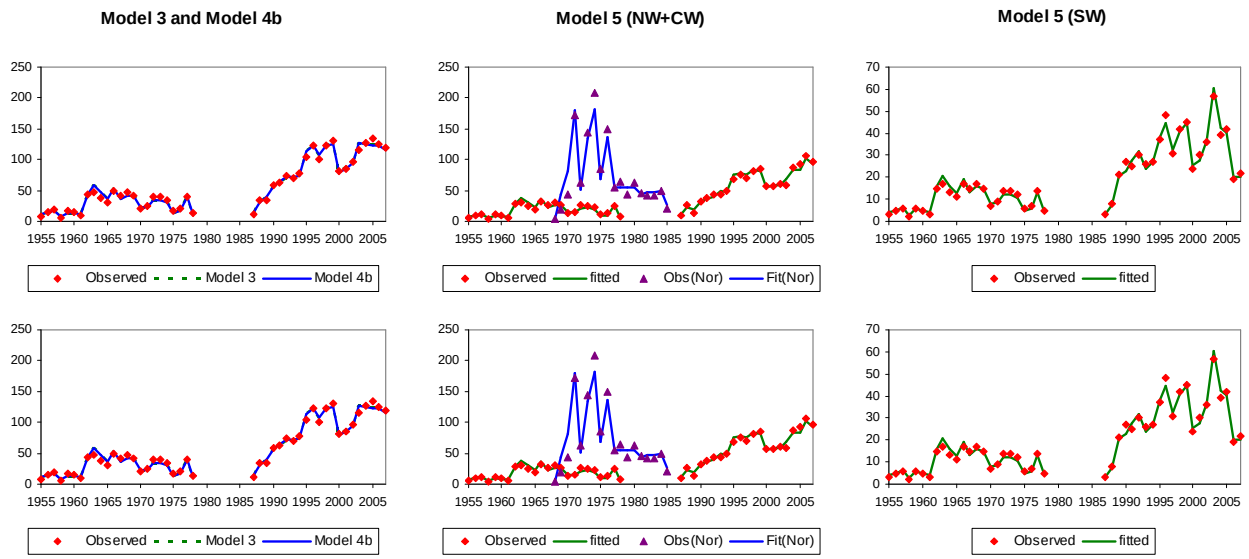

Figure 1. Observed and model estimated female catches for various models for a MSYR value of 1% (top) and 2% (bottom) when the **Brandão likelihood** function is used in the model fitting procedure. Models 5 (NW+CW) 5 (SW) are fitted to different data are therefore shown in different plots.

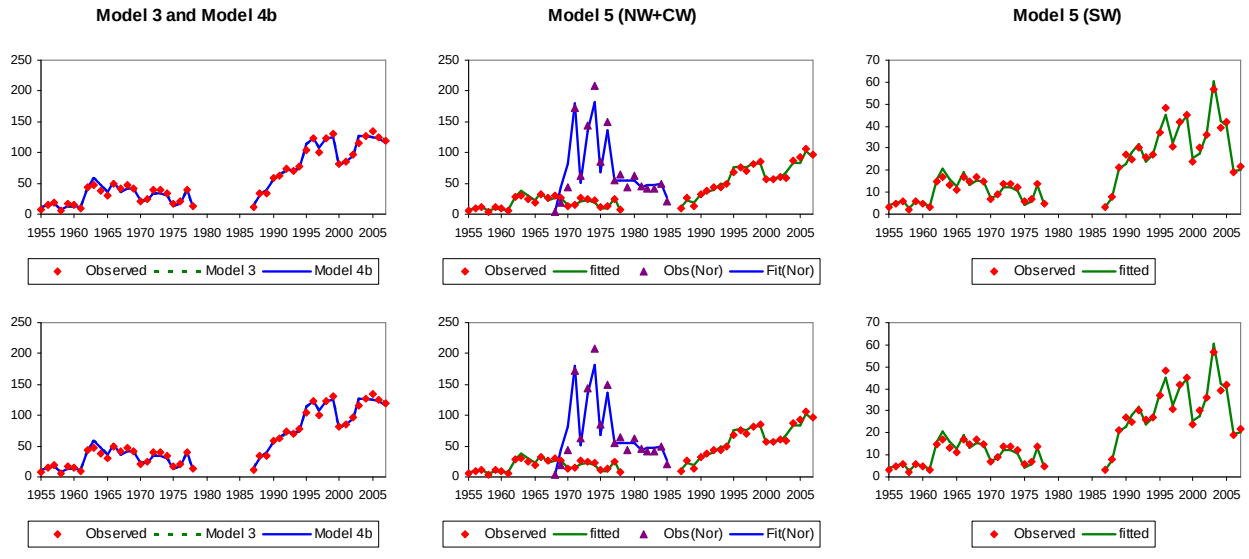

Figure 2. Observed and model estimated female catches for various models for a MSYR value of 1% (top) and 2% (bottom) when the **Schweder likelihood** function is used in the model fitting procedure. Models 5 (NW+CW) 5 (SW) are fitted to different data are therefore shown in different plots.

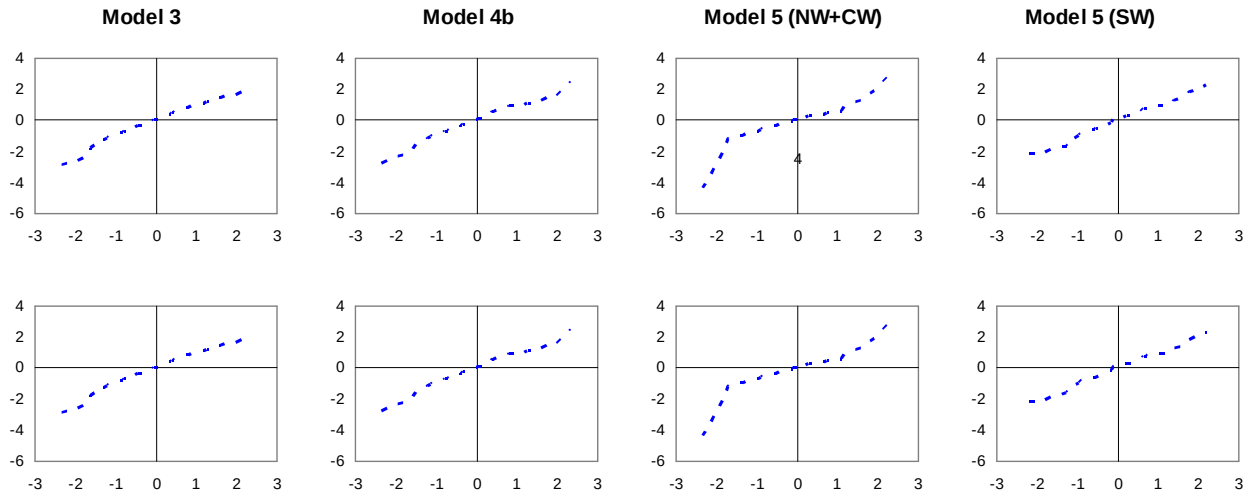

Figure 3. Normal QQ-plots of the standardised residuals (pooled across all three fisheries) for various models for a MSYR value of 1% (top) and 2% (bottom) when the **Brandão likelihood** function is used in the model fitting procedure.

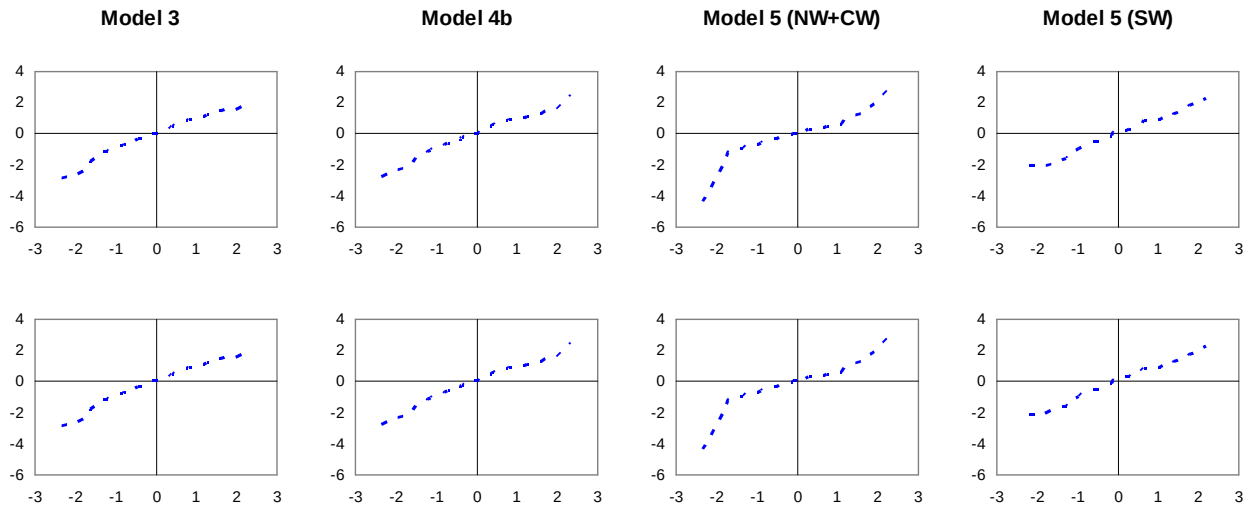

Figure 4. Normal QQ-plots of the standardised residuals (pooled across all three fisheries) for various models for a MSYR value of 1% (top) and 2% (bottom) when the **Schweder likelihood** function is used in the model fitting procedure.

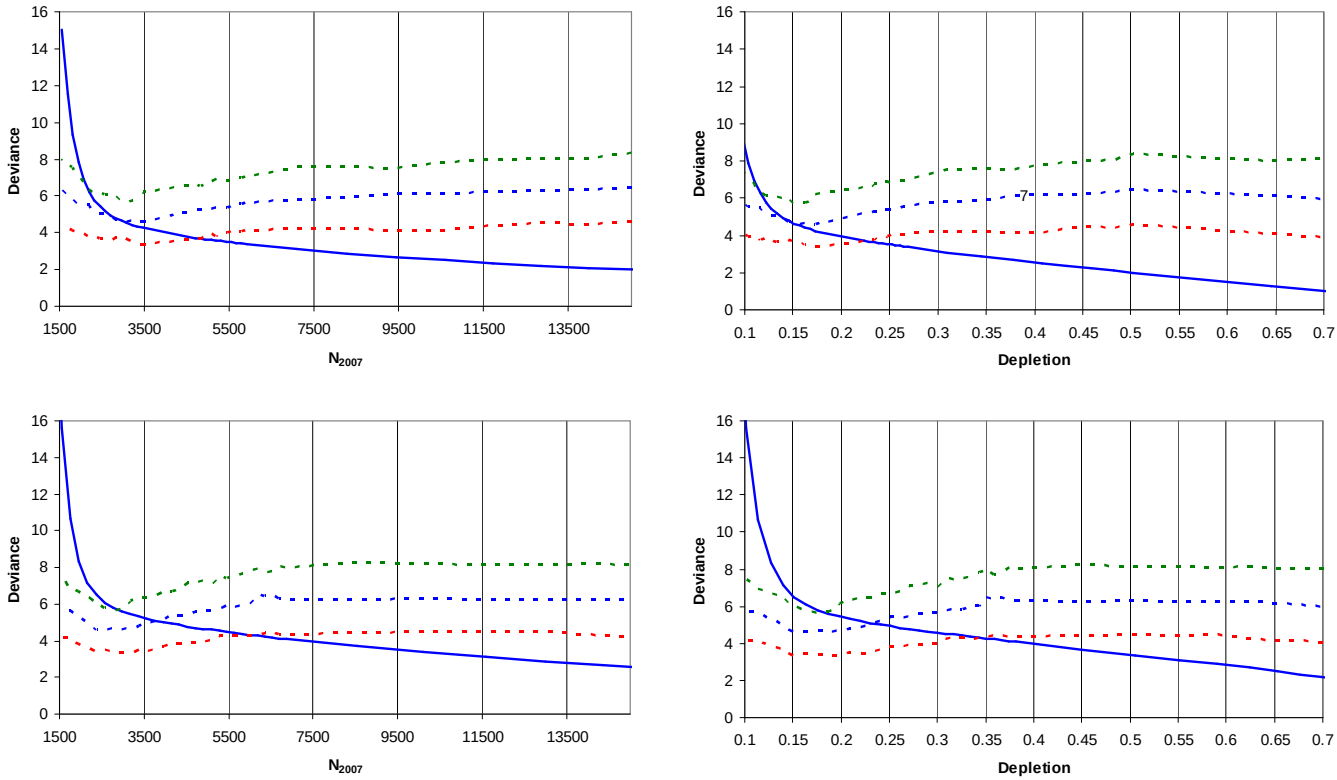

Figure 5. Observed deviance (solid line) and 2.5%, 5% and 10% quantiles (dashed lines) based on 1 000 simulations, for **Model 3** with MSYR = 1% (top) and 2% (bottom) when the **Brandão likelihood** function is used in the model fitting procedure.

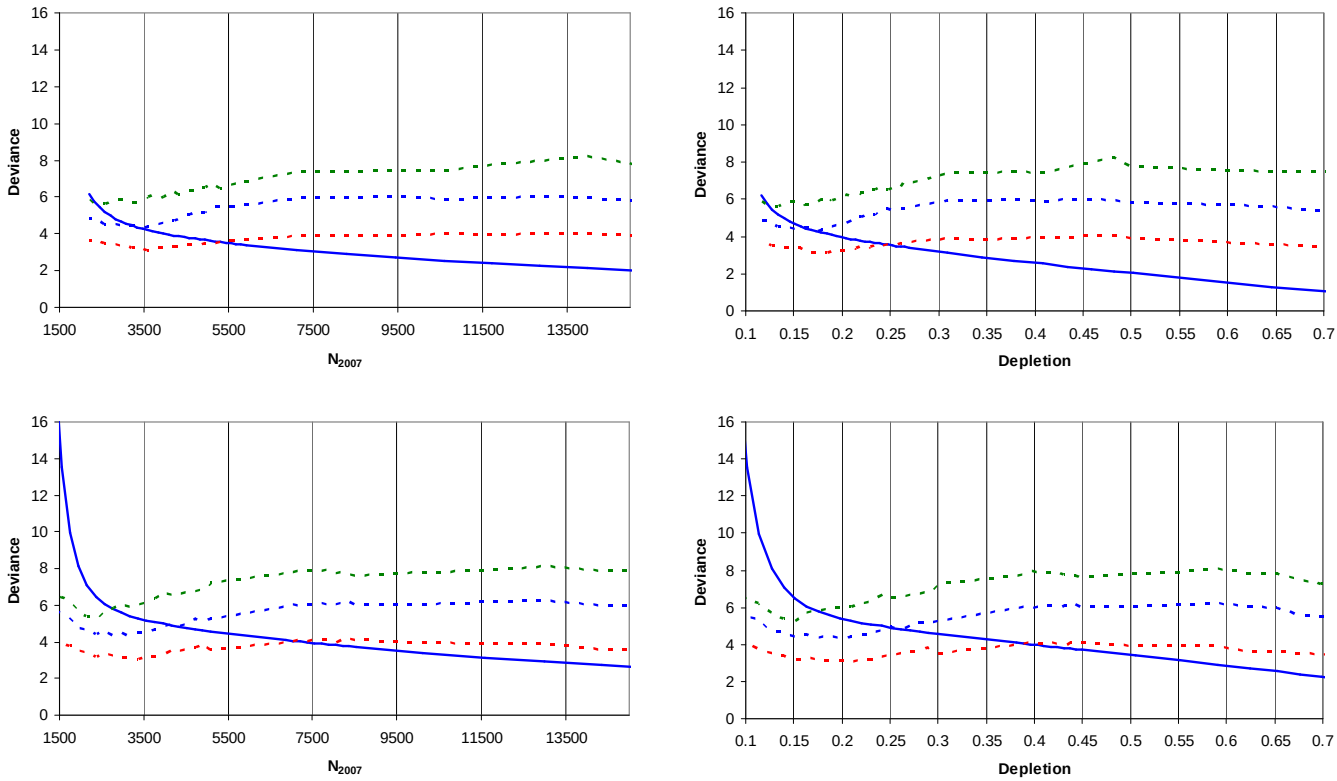

Figure 6. Observed deviance (solid line) and 2.5%, 5% and 10% quantiles (dashed lines) based on 1 000 simulations, for **Model 3** with MSYR = 1% (top) and 2% (bottom) when the **Schweder likelihood** function is used in the model fitting procedure.

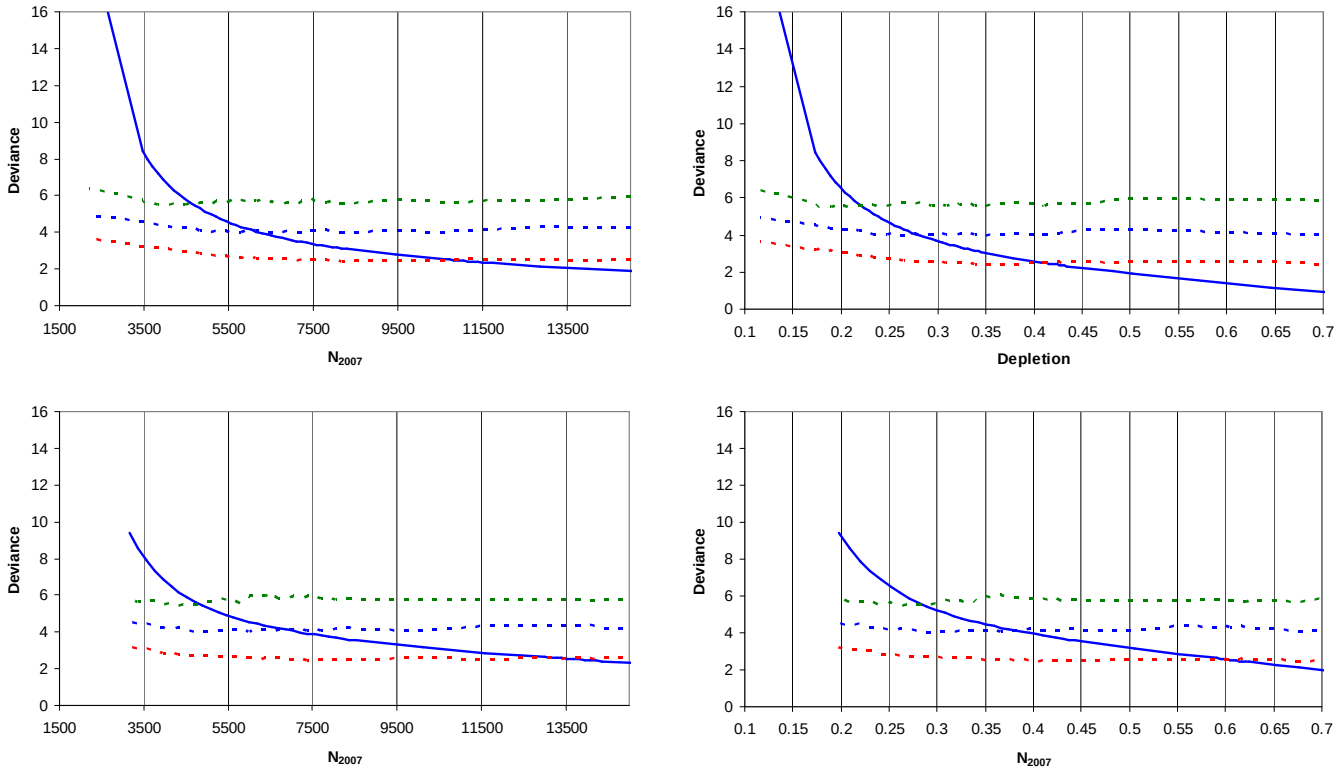

Figure 7. Observed deviance (solid line) and 2.5%, 5% and 10% quantiles (dashed lines) based on 1 000 simulations, for **Model 4b** with MSYR = 1% (top) and 2% (bottom) when the **Brandão likelihood** function is used in the model fitting procedure.

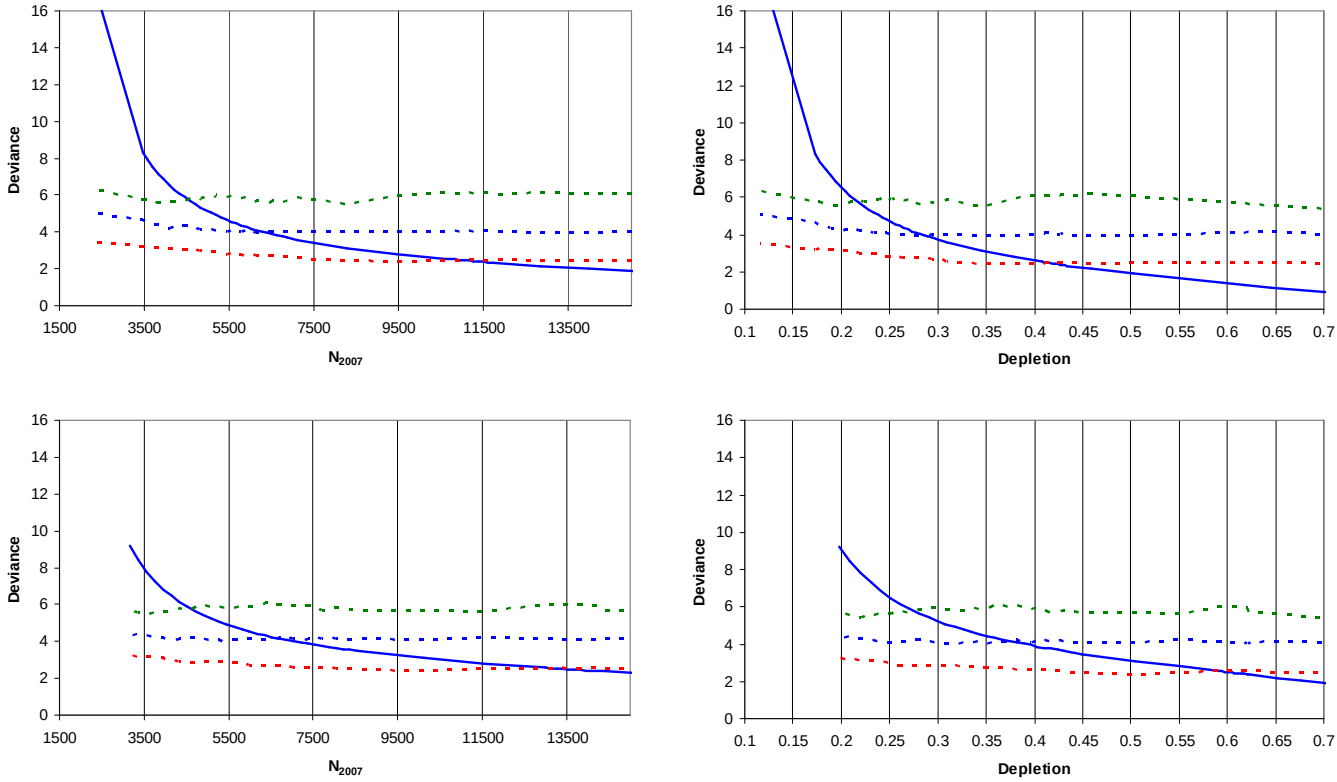

Figure 8. Observed deviance (solid line) and 2.5%, 5% and 10% quantiles (dashed lines) based on 1 000 simulations, for **Model 4b** with MSYR = 1% (top) and 2% (bottom) when the **Schweder likelihood** function is used in the model fitting procedure.

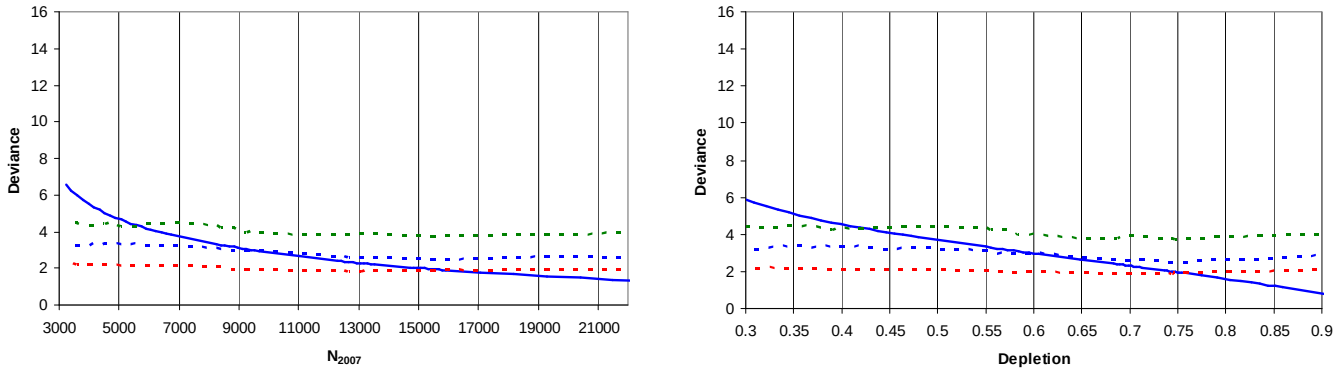

Figure 9. Observed deviance (solid line) and 2.5%, 5% and 10% quantiles (dashed lines) based on 1 000 simulations, for **Model 5 (NW+CW)** with MSYR = 2% when the **Brandão likelihood** function is used in the model fitting procedure.

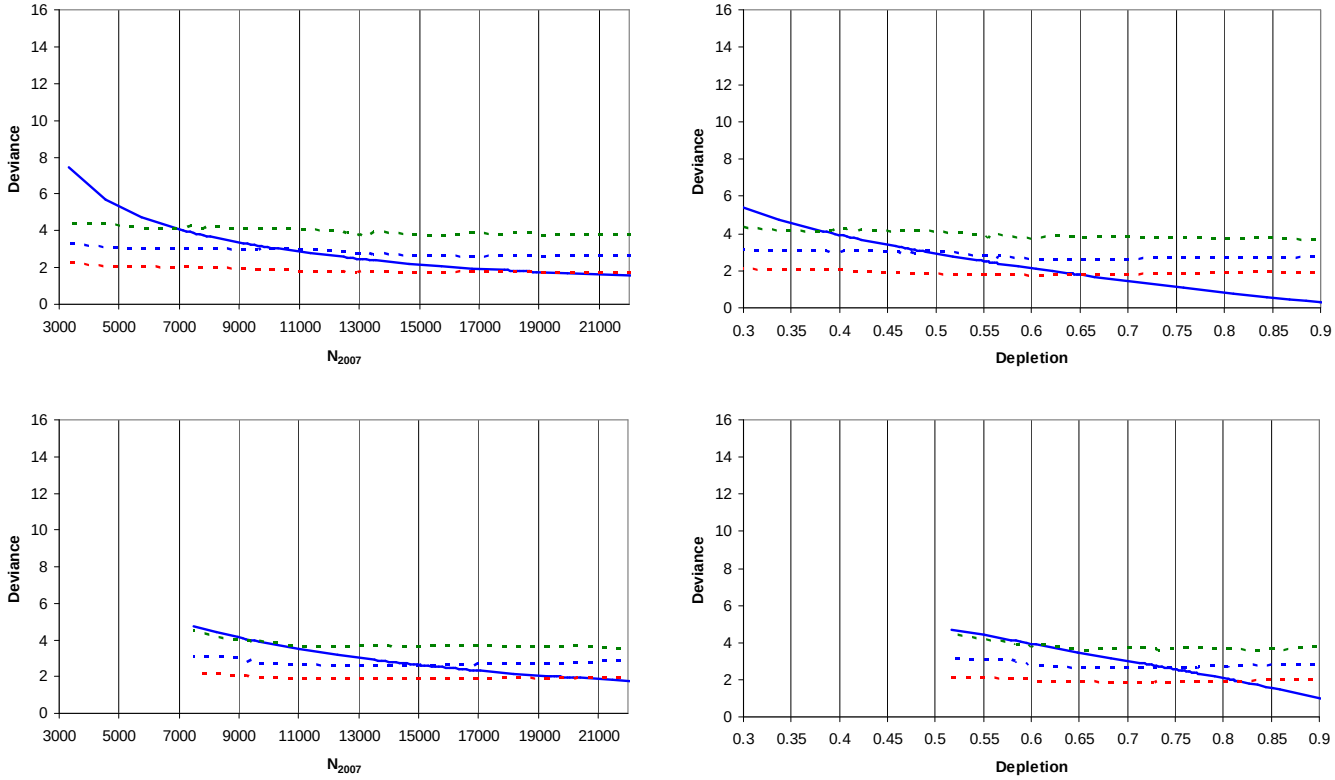

Figure 10. Observed deviance (solid line) and 2.5%, 5% and 10% quantiles (dashed lines) based on 1 000 simulations, for **Model 5 (NW+CW)** with MSYR = 1% (top) and 2% (bottom) when the **Schweder likelihood** function is used in the model fitting procedure.

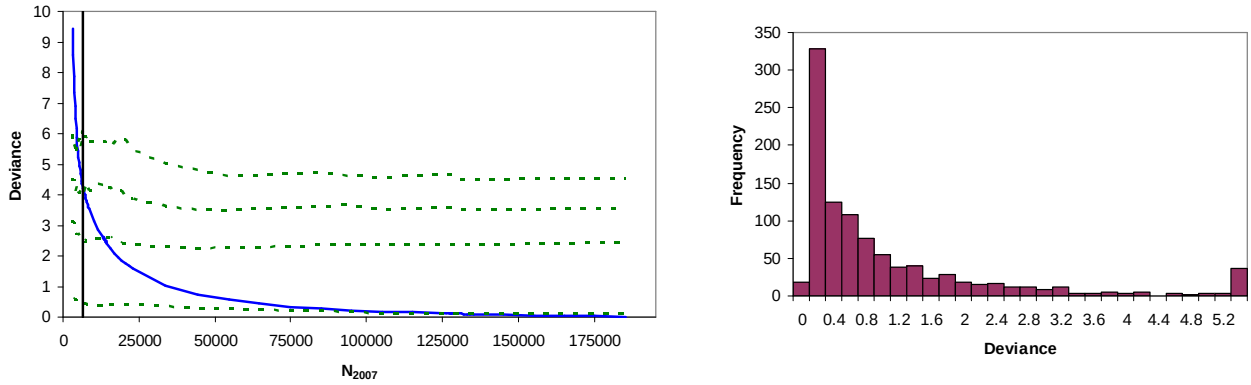

Figure 11. Observed deviance (solid line) and 2.5%, 5%, 10 and 50% quantiles (dashed lines) based on 1 000 simulations, for **Model 4b**, with the **Brandão likelihood** and MSYR = 2%, which has the lowest AIC_c value (amongst the comparable models (Model 3 and Model 4b)) using the **Brandão likelihood** function. The vertical line represents the value of N_{2007} at which the 5% quantile occurs. A histogram of the distribution of the deviances for the 5% quantile is also shown.

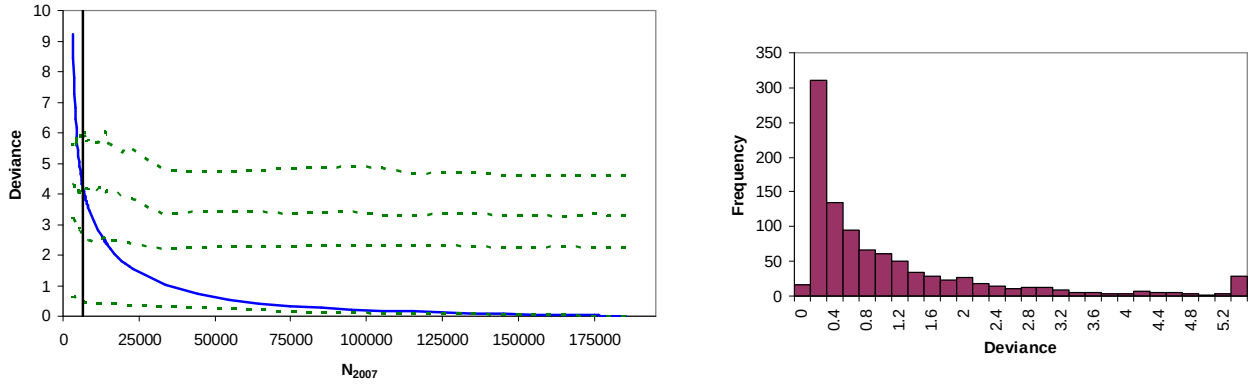

Figure 12. Observed deviance (solid line) and 2.5%, 5%, 10 and 50% quantiles (dashed lines) based on 1 000 simulations, for **Model 4b**, with the **Schweder likelihood** and MSYR = 2%, which has the lowest AIC_c value (amongst the comparable models (Model 3 and Model 4b)) using the **Schweder likelihood** function. The vertical line represents the value of N_{2007} at which the 5% quantile occurs. A histogram of the distribution of the deviances for the 5% quantile is also shown.

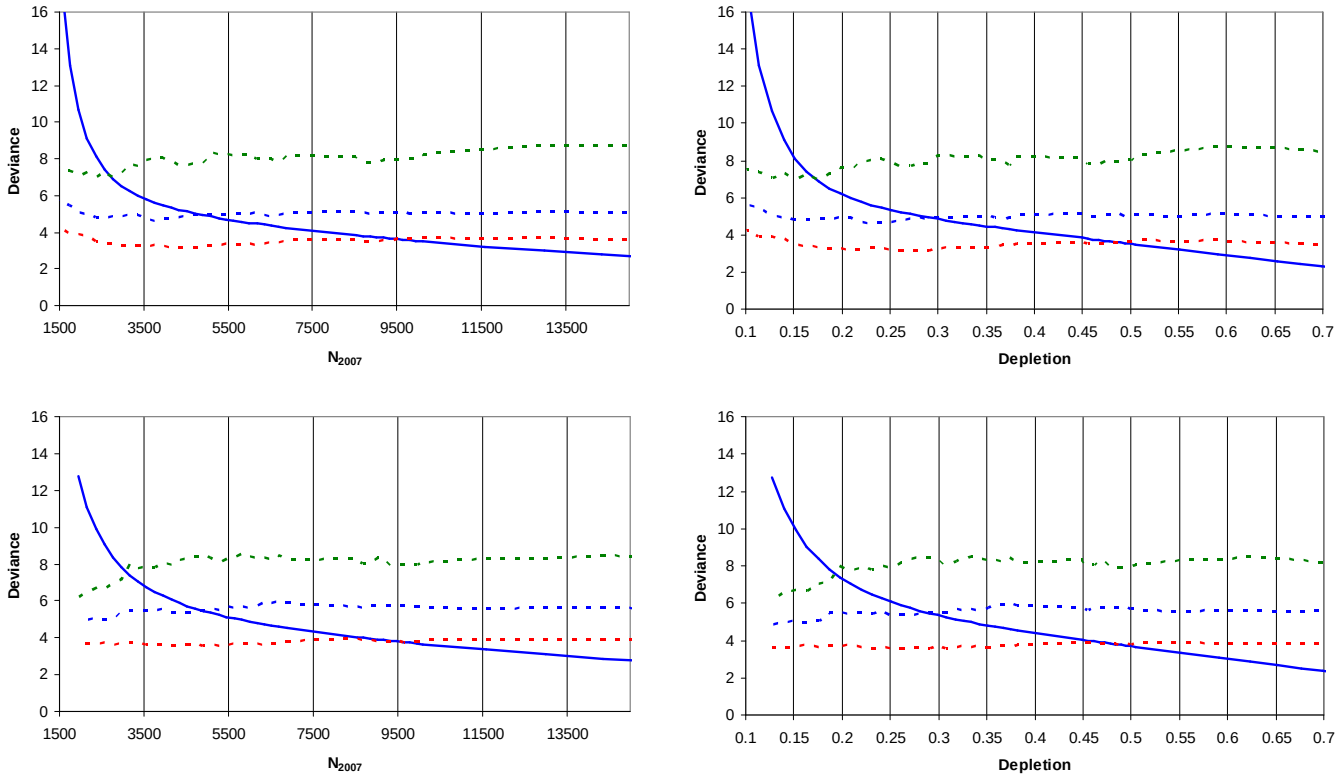

Figure 13. Observed deviance (solid line) and 2.5%, 5% and 10% quantiles (dashed lines) based on 1 000 simulations, for **Model 3** with MSYR = 2% when the Schweder likelihood function is used in the model fitting procedure and the parameter β^f is set to zero (top), and when β^m is set to zero (bottom).

APPENDIX

Simulation algorithm

For the best estimate of virgin biomass (*K*) (here taken to be 200 000 as a surrogate for infinity), the models described in the text are fitted to the original data to obtain estimates for the overdispersion (σ's) and the selectivity of males relative to females (λ's) parameters for the period and whalers concerned. Then for a given value of the true virgin biomass (*K*), and the overdispersion as estimated for *K* = 200 000, the models are fitted to the original data to obtain estimates of the λ's. For each model the deviance as a function of *K* is obtained for the original data.

For each set of values of *K*, *r*, and λ_i, the total annual catches ($C_y = C_y^m + C_y^f$) and the annual reported total catches (C_y^i), the following steps are taken:

1. Set $N_{1948,a}^g = \frac{1}{2}\eta N_a^*$, using equation (5).
2. Generate C_y^f, C_y^m, $C_y^{f(i)}$ and $C_y^{m(i)}$.
3. From $C_{y,a}^g$, project $N_{y,a}^f$ and $N_{y,a}^m$ forward one year (using equations (1) to (3)).
4. Repeat steps (2) and (3) until the end of the time period (i.e. 2007).
5. Fit models to the generated data in which *K* is fixed and for the case when *K* is estimated to get the deviance value for the generated data.
6. Repeat steps (1) to (5) 1000 times to get the distribution of the deviance values.

Data generation

The data generation has to take into account that not all whales are sampled for sex, and that there is a period over which both Norwegian and Greenlandic catches occurred. The assumption has been made that the Norwegian catch was always fully sampled, so that the sampled Greenland catch has to be generated from the total Greenland catch each year.

1] Period 1948–1954 and 1986 (no sampling):

- Generate C_y^f from the normal distribution given by:

$$\mathrm{N}\left(\frac{\sum_a N_{y,a}^f . G_a}{\sum_a N_{y,a}^f . G_a + \lambda^I \sum_a N_{y,a}^m . G_a} C_y, \sigma_I^2 \frac{\sum_a N_{y,a}^f . G_a}{\sum_a N_{y,a}^f . G_a + \lambda^I \sum_a N_{y,a}^m . G_a} C_y \right), \qquad \text{(A.1)}$$

  i.e. the λ^i and σ_i correspond to the Greenlandic (1955-1978) period.

- The total number of males is then given by $C_y^m = C_y - C_y^f$.

2] Period 1955–1967 (only Greenland catch, which is sampled):

- Generate C_y^f and C_y^m as in (A.1) above.
- Sample C_y^I without replacement and with autocorrelation ρ from C_y with sex split given by C_y^f and C_y^m, to get sampled numbers $C_y^{f(I)}$ and $C_y^{m(I)}$.

3] Period 1968–1978 (both Greenland and Norwegian catches, both sampled):

- Generate the Norwegian catch $C_y^{f(II)}$ from the normal distribution given by:

$$\mathrm{N}\left(\frac{\sum_a N_{y,a}^f . G_a}{\sum_a N_{y,a}^f . G_a + \lambda^{II} \sum_a N_{y,a}^m . G_a} C_y^{II}, \sigma_{II}^2 \frac{\sum_a N_{y,a}^f . G_a}{\sum_a N_{y,a}^f . G_a + \lambda^{II} \sum_a N_{y,a}^m . G_a} C_y^{II} \right)$$

- The total number of males caught by the Norwegians is then given by $C_y^{m(II)} = C_y^{II} - C_y^{f(II)}$.
- Note that the Greenland catch is $C_y - C_y^{II}$, to be comprised of $C_y^{f(I)*}$ females and $C_y^{m(I)*}$ males.
- Generate $C_y^{f(I)*}$ from the normal distribution given by:

$$\mathrm{N}\left(\frac{\sum_a N_{y,a}^f . G_a}{\sum_a N_{y,a}^f . G_a + \lambda^{I} \sum_a N_{y,a}^m . G_a} \left(C_y - C_y^{II}\right), \sigma_I^2 \frac{\sum_a N_{y,a}^f . G_a}{\sum_a N_{y,a}^f . G_a + \lambda^{I} \sum_a N_{y,a}^m . G_a} \left(C_y - C_y^{II}\right) \right)$$

- The total number of males caught by Greenland is then given by $C_y^{m(I)*} = \left(C_y - C_y^{II}\right) - C_y^{f(I)*}$.
- Sample without replacement and with autocorrelation from $C_y - C_y^{II}$ with sex split given by $C_y^{f(I)*}$ and $C_y^{m(I)*}$, to give the whales caught and sampled by Greenland $C_y^{f(I)}$ and $C_y^{m(I)}$.
- Add the $C_y^{f(I)*}$ and $C_y^{m(I)*}$ to the Norwegian generated catches to get the total catches by sex (e.g. $C_y^f = C_y^{f(II)} + C_y^{f(I)*}$).

4] Period 1979–1985 (both Greenland and Norwegian catches; the former is not sampled, but is assumed to be governed by the parameters for the first (1955–1978) period of sampled Greenland catches):

- Generate the Norwegian catch $C_y^{f(II)}$ from the normal distribution given by:

$$\mathrm{N}\left(\frac{\sum_a N^f_{y,a}.G_a}{\sum_a N^f_{y,a}.G_a + \lambda^{II}\sum_a N^m_{y,a}.G_a} C^{II}_y, \sigma^2_{II} \frac{\sum_a N^f_{y,a}.G_a}{\sum_a N^f_{y,a}.G_a + \lambda^{II}\sum_a N^m_{y,a}.G_a} C^{II}_y\right)$$

- The total number of males caught by the Norwegians is then given by $C^{m(II)}_y = C^{II}_y - C^{f(II)}_y$.
- Note that the Greenland catch is $C_y - C^{II}_y$, to be comprised of $C^{f(I)*}_y$ females and $C^{m(I)*}_y$ males.
- Generate $C^{f(I)*}_y$ from the normal distribution given by:

$$\mathrm{N}\left(\frac{\sum_a N^f_{y,a}.G_a}{\sum_a N^f_{y,a}.G_a + \lambda^{I}\sum_a N^m_{y,a}.G_a} \left(C_y - C^{II}_y\right), \sigma^2_{I} \frac{\sum_a N^f_{y,a}.G_a}{\sum_a N^f_{y,a}.G_a + \lambda^{I}\sum_a N^m_{y,a}.G_a} \left(C_y - C^{II}_y\right)\right)$$

- The total number of males caught by Greenland is then given by $C^{m(I)*}_y = \left(C_y - C^{II}_y\right) - C^{f(I)*}_y$.
- Add the $C^{f(I)*}_y$ and $C^{m(I)*}_y$ to the Norwegian generated catches to get the total catches by sex (e.g. $C^f_y = C^{f(II)}_y + C^{f(I)*}_y$).

5] Period 1987–2007 (only Greenland catch, which is sampled):

- Generate C^f_y from normal distribution given by:

$$\mathrm{N}\left(\frac{\sum_a N^f_{y,a}.G_a}{\sum_a N^f_{y,a}.G_a + \lambda^{III}\sum_a N^m_{y,a}.G_a} C_y, \sigma^2_{III} \frac{\sum_a N^f_{y,a}.G_a}{\sum_a N^f_{y,a}.G_a + \lambda^{III}\sum_a N^m_{y,a}.G_a} C_y\right).$$

- The total number of males is then given by $C^m_y = C_y - C^f_y$.
- Sample C^{III}_y randomly without replacement from C_y with sex split given by C^f_y and C^m_y, to get sampled numbers $C^{f(III)}_y$ and $C^{m(III)}_y$.

In the data generation algorithm described above, in instances in which a negative catch was generated for one of the sexes, the catch for that sex was set to zero and consequently the catch for the opposite sex was set to the total number being sampled (as otherwise in this case, a catch greater than the number being sampled would have been generated to compensate for the negative generated catch).

Modifications for new applications of this paper

The data generation algorithm described above applies to Model 5, where the total catches and the reported catches refer to those in the NW+CW strata. All the Norwegian catches are assumed to

come from the NW+CW population. The catches in the earlier Greenlandic period are split by area by taking males and females separately, calculating the average ratio of the total Greenlandic catch of NW+CW to SW over the years of the later Greenlandic period, and then applying this ratio to the earlier period for which this split is not known. In other respects, the specification of Model 5 follows the prescription given in IWC (2008a).

For the other models considered in this paper, the following alterations to the data generation algorithm were made:

Model 4b: In Step 3 and in Step 4, the Norwegian catches are not generated but the observed Norwegian data is used (assuming that all Norwegian catches were sampled). Therefore the following changes are made:

$$\begin{aligned} C_y^{II} &\rightarrow C_y^{Norwegian} \\ C_y^{f(II)} &\rightarrow C_y^{f(Norwegian)} \\ C_y^{m(II)} &\rightarrow C_y^{m(Norwegian)} \end{aligned} .$$

In Step 5, the total Greenland catches (C_y) have to be split into the NW+CW and SW strata (C_y^{NW+CW} and C_y^{SW}), where these are taken to be the observed data as used for Model 5(NW+CW) and Model 5 (SW). Step 5 is thus changed into:

- Generate $C_y^{f(NW+CW)}$ from normal distribution given by:

$$N\left(\frac{\sum_a N_{y,a}^f.G_a}{\sum_a N_{y,a}^f.G_a + \lambda^{II(NW+CW)}\sum_a N_{y,a}^m.G_a} C_y^{NW+CW}, \sigma_{II(NW+CW)}^2 \frac{\sum_a N_{y,a}^f.G_a}{\sum_a N_{y,a}^f.G_a + \lambda^{II(NW+CW)}\sum_a N_{y,a}^m.G_a} C_y^{NW+CW}\right)$$

where

.

- The total number of males is then given by $C_y^{m(NW+CW)} = C_y^{NW+CW} - C_y^{f(NW+CW)}$.
- Sample $C_y^{II(NW+CW)}$ randomly without replacement from C_y^{NW+CW} with sex split given by $C_y^{f(NW+CW)}$ and $C_y^{m(NW+CW)}$, to get sampled numbers $C_y^{f(II(NW+CW))}$ and $C_y^{m(II(NW+CW))}$.
- Generate $C_y^{f(SW)}$ from normal distribution given by:

$$N\left(\frac{\sum_a N_{y,a}^f.G_a}{\sum_a N_{y,a}^f.G_a + \lambda^{III(SW)}\sum_a N_{y,a}^m.G_a} C_y^{SW}, \sigma_{III(SW)}^2 \frac{\sum_a N_{y,a}^f.G_a}{\sum_a N_{y,a}^f.G_a + \lambda^{III(SW)}\sum_a N_{y,a}^m.G_a} C_y^{SW}\right), \text{ where}$$

$$\lambda^{III(SW)} = \lambda_{87}\left(2007 - y\right)/(2007 - 1987) + \lambda_{06}\left(y - 1987\right)/(2007 - 1987),$$

i.e. λ is assumed to change linearly over time during this period.

- The total number of males is then given by $C_y^{m(SW)} = C_y^{SW} - C_y^{f(SW)}$.
- Sample $C_y^{II(SW)}$ randomly without replacement from C_y^{SW} with sex split given by $C_y^{f(SW)}$ and $C_y^{m(SW)}$, to get sampled numbers $C_y^{f(III(SW))}$ and $C_y^{m(III(SW))}$.
- Get total catches by sex by adding the catches by sex from each strata (e.g. $C_y^f = C_y^{f(II(NW+CW))} + C_y^{f(III(SW))}$

Model 3: The data generation algorithm remains essentially the same as for Model 4b, but with the following changes:

- When generating data for the NW+CW strata:

$$\sum_a N_{y,a}^f . G_a \rightarrow \sum_a N_{y,a}^f . G_a \left(A^f\right)$$
$$\sum_a N_{y,a}^m . G_a \rightarrow \sum_a N_{y,a}^m . G_a \left(A^m\right), \text{ where}$$

$$A^f = \frac{e^{\left(\alpha^f + \beta^f y\right)}}{1 - e^{\left(\alpha^f + \beta^f y\right)}}$$

$$A^m = \frac{e^{\left(\alpha^m + \beta^m y\right)}}{1 - e^{\left(\alpha^m + \beta^m y\right)}}$$

- When generating data for the SW strata:

$$\sum_a N_{y,a}^f . G_a \rightarrow \sum_a N_{y,a}^f . G_a \left(1 - A^f\right)$$
$$\sum_a N_{y,a}^m . G_a \rightarrow \sum_a N_{y,a}^m . G_a \left(1 - A^m\right)$$

Because of time limitations the issue of the above procedure generating the sex-sampled catch yielded with less variability (in median terms) than the original data has not been investigated further. Hence in this document the autocorrelation has been set to zero.